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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      January 24, 2006, 05:25:18 ; Search time 1497 Seconds
                                  (without alignments)
                              9793.993 Million cell updates/sec

Title:           US-10-808-964A-2
Perfect score:   1773
Sequence:        1 ggtacctccgtggattgtc..........caaatcggccttcgggtacc 1773

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters:    19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published Applications NA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1773	100.0	1773	6	US-10-314-512-2	Sequence 2, Appli
2		1773	100.0	1773	8	US-10-808-964-2	Sequence 2, Appli
3	c	1285.2	72.5	1768	7	US-10-311-423-4	Sequence 4, Appli
4	c	1278.8	72.1	1768	7	US-10-311-423-2	Sequence 4, Appli
5	c	1277.2	72.0	1768	7	US-10-311-423-6	Sequence 6, Appli
6	c	1274	71.9	1768	7	US-10-311-423-3	Sequence 3, Appli
7	c	1274	71.9	1768	7	US-10-311-423-5	Sequence 1, Appli
8	c	1252	70.6	1762	7	US-10-311-423-1	Sequence 1, Appli
9	c	1218.2	68.7	1759	7	US-10-311-423-7	Sequence 7, Appli
10	c	1196.8	67.5	7460	5	US-10-038-001-7	Sequence 16, Appli
11	c	1195.8	67.4	5225	6	US-10-286-186-16	Sequence 16, Appl
12	c	1195.8	67.4	5285	5	US-10-038-001-1	Sequence 1, Appli
13	c	1195.8	67.4	5650	5	US-10-038-001-2	Sequence 2, Appli
14	c	1195.8	67.4	5650	6	US-10-286-186-17	Sequence 17, Appl
15	c	1059.8	59.8	1759	3	US-09-784-962-5	Sequence 5, Appli
16	c	1059.8	59.8	1759	8	US-09-884-514-5	Sequence 5, Appli
17	c	1059.8	59.8	1759	8	US-10-624-049-5	Sequence 5, Appli
18	c	1059.8	59.8	1759	9	US-10-780-318-5	Sequence 5, Appli
19	c	1058.4	59.7	1768	6	US-10-314-512-1	Sequence 1, Appli
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23	c	981.2	55.3	1768	8	US-10-624-049-3	Sequence 3, Appli
24	c	981.2	55.3	1768	9	US-10-780-318-3	Sequence 3, Appli
25	c	976.4	55.1	1768	3	US-09-784-962-4	Sequence 4, Appli
26	c	976.4	55.1	1768	8	US-09-884-514-4	Sequence 4, Appli
27	c	976.4	55.1	1768	8	US-10-624-049-4	Sequence 4, Appli
28	c	976.4	55.1	1768	9	US-10-780-318-4	Sequence 4, Appli
29	c	967.2	54.6	1768	3	US-09-884-514-6	Sequence 6, Appli
30	c	967.2	54.6	1768	8	US-10-624-049-6	Sequence 6, Appli
31	c	954	53.8	1767	9	US-10-780-318-6	Sequence 6, Appli
32	c	954	53.8	1767	3	US-09-784-962-1	Sequence 1, Appli
33	c	954	53.8	1767	8	US-09-884-514-1	Sequence 1, Appli
34	c	954	53.8	1767	8	US-10-624-049-1	Sequence 1, Appli
35	c	954	53.8	1767	9	US-10-780-318-1	Sequence 1, Appli
36	c	952.4	53.7	1767	3	US-09-784-962-2	Sequence 2, Appli
37	c	952.4	53.7	1767	8	US-09-884-514-2	Sequence 2, Appli
38	c	952.4	53.7	1767	8	US-10-624-049-2	Sequence 2, Appli
39	c	952.4	53.7	1767	9	US-10-780-318-2	Sequence 2, Appli
40	c	921	51.9	1759	7	US-10-682-420-5	Sequence 5, Appli
41	c	921	51.9	1759	7	US-10-409-613-5	Sequence 5, Appli
42	c	921	51.9	1759	7	US-10-442-180-5	Sequence 5, Appli
43	c	921	51.9	1759	8	US-10-718-266-5	Sequence 5, Appli
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ALIGNMENTS

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US-10-314-512-2
; Sequence 2, Application US/10314512
; Publication No. US20030170270A1
; GENERAL INFORMATION:
;  APPLICANT: Meng, Xiang-Jin
;  APPLICANT: Fenaux, Martijn
;  APPLICANT: Halbur, Patrick G.
;  TITLE OF INVENTION: Chimeric Infectious DNA Clones, Chimeric Porcine Circoviruses and
;  TITLE OF INVENTION:  Thereof
;  FILE REFERENCE: AM100878
;  CURRENT APPLICATION NUMBER: US/10/314,512
;  CURRENT FILING DATE:  2002-12-09
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;  LENGTH: 1773
;  TYPE: DNA
;  ORGANISM: Porcine circovirus
US-10-314-512-2

Query Match              100.0%;  Score 1773;  DB 6;  Length 1773;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 1773; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    301 CAGTAGGTGTCCCTAGGCTCAGCAAAATTACGGGCCCACTGGCTCTTCCCACAACCGGGC 360
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OM nucleic - nucleic search, using sw model

Run on:   January 24, 2006, 05:06:16 ; Search time 333 Seconds
                                       (without alignments)
                              9464.315 Million cell updates/sec

Title:          US-10-808-964A-2
Perfect score:  1773
Sequence:       1 ggtacctccgtggatggtc..........caaatcggcctcgggtacc 1773

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters:   2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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c 2	1059.8	59.8	1759	3	US-09-082-558-5	Sequence 5, Appli
c 3	1059.8	59.8	1759	3	US-09-161-092-5	Sequence 5, Appli
c 4	1059.8	59.8	1759	3	US-09-583-350-5	Sequence 5, Appli
c 5	1059.8	59.8	1759	3	US-09-784-962-5	Sequence 5, Appli
c 6	1059.8	59.8	1759	3	US-09-784-962-5	Sequence 5, Appli
c 7	1053.2	59.4	3609	3	US-09-583-545-13	Sequence 13, Appl
c 8	981.2	55.3	1768	3	US-09-347-594-3	Sequence 3, Appli
c 9	981.2	55.3	1768	3	US-09-082-558-3	Sequence 3, Appli
c 10	981.2	55.3	1768	3	US-09-161-092-3	Sequence 3, Appli
c 11	981.2	55.3	1768	3	US-09-583-350-3	Sequence 3, Appli
c 12	981.2	55.3	1768	3	US-09-082-558-3	Sequence 3, Appli
c 13	981.2	55.3	1768	3	US-09-784-962-3	Sequence 3, Appli
c 14	976.4	55.1	1768	3	US-09-347-594-4	Sequence 4, Appli
c 15	976.4	55.1	1768	3	US-09-082-558-4	Sequence 4, Appli
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c 17	976.4	55.1	1768	3	US-09-583-350-4	Sequence 4, Appli
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c 22	967.2	54.6	1768	3	US-09-583-350-6	Sequence 6, Appli
c 23	967.2	54.6	1768	3	US-09-884-514-6	Sequence 6, Appli
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c 25	954	53.8	1767	3	US-09-082-558-1	Sequence 1, Appli
c 26	954	53.8	1767	3	US-09-161-092-1	Sequence 1, Appli
c 27	954	53.8	1767	3	US-09-583-350-1	Sequence 1, Appli
c 28	954	53.8	1767	3	US-09-884-514-1	Sequence 1, Appli
c 29	954	53.8	1767	3	US-09-784-962-1	Sequence 1, Appli
c 30	952.4	53.7	1767	3	US-09-347-594-2	Sequence 2, Appli
c 31	952.4	53.7	1767	3	US-09-082-558-2	Sequence 2, Appli
c 32	952.4	53.7	1767	3	US-09-161-092-2	Sequence 2, Appli
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c 35	952.4	53.7	1767	3	US-09-784-962-2	Sequence 2, Appli
c 36	921	51.9	1759	3	US-09-514-245-5	Sequence 5, Appli
c 37	919.4	51.9	1759	3	US-09-514-245-1	Sequence 1, Appli
c 38	916.2	51.7	1759	3	US-09-267-177-38	Sequence 38, Appl
c 39	916.2	51.7	1759	3	US-09-267-177-40	Sequence 40, Appl
c 40	914.6	51.6	1759	3	US-09-514-245-163	Sequence 163, App
c 41	906.6	51.1	1759	3	US-09-514-245-164	Sequence 164, App
c 42	904.2	51.0	1727	3	US-09-267-177-2	Sequence 2, Appli
c 43	879.2	49.6	1674	3	US-09-267-177-1	Sequence 1, Appli
c 44	875	49.4	939	3	US-09-514-245-9	Sequence 9, Appli
c 45	870.2	49.1	936	3	US-09-267-177-20	Sequence 20, Appli

ALIGNMENTS

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RESULT 1
US-09-347-594-5/c
; Sequence 5, Application US/09347594
; Patent No. 6217883
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon M.
; APPLICANT: MEEHAN, Brian M.
; APPLICANT: ELLIS, John A.
; APPLICANT: KRAKOWKA, George S.
; APPLICANT: AUDONNET, Jean-Christophe F.
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE
; FILE REFERENCE: 454313-2338
; CURRENT APPLICATION NUMBER: US/09/347,594
; CURRENT FILING DATE: 1999-07-01
; EARLIER APPLICATION NUMBER: 98 08777
; EARLIER FILING DATE: 1998-07-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-347-594-5

Query Match             59.8%;  Score 1059.8;  DB 3;  Length 1759;
Best Local Similarity   90.5%;  Pred. No. 0;
Matches 1156;  Conservative    0;  Mismatches  112;  Indels    9;  Gaps    2;

Qy      1 GGTACCTCCGTGGATTGTTCTCCAGCAGTCTTCCAAAATTGCAAAGTAGTAATCCTCCGA 60
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 CTGGTAATCAAAATACTGCGGGCCAAAAAGGAACAGTACCCCCTTTAGTCTTCTACAGTC 180
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                  GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:   January 24, 2006, 05:14:52 ; Search time 7316 Seconds
                                       (without alignments)
                        11338.641 Million cell updates/sec

Title:          US-10-808-964a-2
Perfect score:  1773
Sequence:       1 ggtaccctccgtggattgttc........caaatcggcctccgggtacc 1773

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:   82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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             3: gb_est3:*
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             6: gb_est5:*
             7: gb_est6:*
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            10: gb_gss2:*
            11: gb_gss3:*
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Result NO.		Score	Query Match	Length	DB	ID	Description
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c	3	48.6	2.7	870	2	BG445569	BG445569 GA_Ea002
c	4	48.2	2.7	573	6	CD659610	CD659610 BtESTef53
c	5	47.6	2.7	1141	10	AG365778	AG365778 Mus muscu
c	6	47.4	2.7	922	10	CNS0073W	AL066784 Drosophil
c	7	47.2	2.7	912	10	AG886740	AG886740 Oryza sat
c	8	46.8	2.6	451	7	CO856405	CO856405 LM_SL5_00
c	9	46.8	2.6	553	7	CO824976	CO824976 LM_GB5_00
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c	12	46.6	2.6	909	10	CNS00JTL	AL076720 Drosophil
c	13	46.4	2.6	560	6	CA222795	CA222795 SCEZFL403
c	14	46	2.6	401	1	AW255252	AW255252 ML252 pep
c	15	45.6	2.6	179	7	CF963096	CF963096 8886rsice
c	16	45.6	2.6	388	7	CF962795	CF962795 7934rsice
c	17	45.6	2.6	389	7	CF962731	CF962731 7773rsice
c	18	45.6	2.6	474	7	CF959714	CF959714 7736rsice
c	19	45.4	2.6	439	8	DN145761	DN145761 4836_G12
c	20	45.2	2.6	330	8	DR179060	DR179060 RTMNUT1_1
c	21	45.2	2.5	415	8	DR012815	DR012815 HRAT1_15
c	22	45.2	2.5	455	8	DN458173	DN458173 EST953972
c	23	460	7.	45.2	2.5	CV144191	CV144191 EST855400
c	24	486	8	45.2	2.5	DR089500	DR089500 RTAL1_9 C
c	25	522	8	45.2	2.5	DN459245	DN459245 EST955044
c	26	540	8	45.2	2.5	DN447345	DN447345 EST943144
c	27	621	7	45.2	2.5	CV137364	CV137364 EST848573
c	28	626	8	45.2	2.5	DN460355	DN460355 EST956154
c	29	649	7	45.2	2.5	CV138441	CV138441 EST849650
c	30	657	7	45.2	2.5	DN458986	DN458986 EST954785
c	31	670	7	45.2	2.5	CN784300	CN784300 EST782991
c	32	703	8	45.2	2.5	DN447213	DN447213 EST943012
c	33	708	8	45.2	2.5	DN462364	DN462364 EST958163
c	34	713	8	45.2	2.5	DN460425	DN460425 EST956224
c	35	724	8	45.2	2.5	DN449051	DN449051 EST944850
c	36	727	7	45.2	2.5	CV137577	CV137577 EST848786
c	37	729	7	45.2	2.5	CV146884	CV146884 EST858093
c	38	739	8	45.2	2.5	DN463011	DN463011 EST958810
c	39	744	8	45.2	2.5	CO413802	CO413802 EST844187
c	40	745	8	45.2	2.5	DN451000	DN451000 EST946799
c	41	757	7	45.2	2.5	CO409276	CO409276 EST839661
c	42	766	8	45.2	2.5	DN451374	DN451374 EST947173
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ALIGNMENTS

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LOCUS       CNS00LT2        1101 bp    DNA        linear   GSS 14-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
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            fly), genomic survey sequence.
ACCESSION   AL078714
VERSION     AL078714.1  GI:5102004
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp; the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1..1101
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR48P19"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    January 24, 2006, 01:18:23 ; Search time 1095 Seconds
                                (without alignments)
                             10791.324 Million cell updates/sec

Title:           US-10-808-964A-2
Perfect score:   1773
Sequence:        1 ggtacctccgtggattgttc.........caaatcggccttcgggtacc 1773

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters:    9993994

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_21:*
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                 2: geneseqn19908:*
                 3: geneseqn20008:*
                 4: geneseqn2001a8:*
                 5: geneseqn2001b8:*
                 6: geneseqn2002a8:*
                 7: geneseqn2002b8:*
                 8: geneseqn2003a8:*
                 9: geneseqn2003b8:*
                10: geneseqn2003c8:*
                11: geneseqn2003d8:*
                12: geneseqn2004a8:*
                13: geneseqn2004b8:*
                14: geneseqn20058:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	1773	100.0	1773	9	AAL57177	Aal57177 Porcine c
c 2	1296.4	73.1	1767	13	ADW76756	Adw76756 Pig circu
c 3	1285.2	72.5	1768	6	ABX08205	Abx08205 PMWS-Porc
c 4	1278.4	72.1	1768	6	ABX08203	Abx08203 PMWS-Porc
c 5	1277.2	72.0	1768	6	ABX08207	Abx08207 CT-Porcin
c 6	1274	71.9	1768	6	ABX08206	Abx08206 CT-Porcin
c 7	1274	71.9	1768	6	ABX08219	Abx08219 PMWS-Porc
c 8	1270.8	71.7	1774	6	ABX08202	Abx08202 PMWS-Porc
c 9	1252	70.6	1762	6	ABX08208	Abx08208 CT-Porcin
c 10	1218.2	68.7	1759	6	ABX08220	Abx08220 PK-15-Por
c 11	1210.2	68.3	1759	4	AAH74867	Aah74867 Nucleotid
c 12	1196.8	67.5	7460	8	ABX94361	Abx94361 Rolling c
c 13	1196.8	67.5	7460	8	AAH74865	Aah74865 Nucleotid
c 14	1195.8	67.4	5285	4	ABX94355	Abx94355 Rolling c
c 15	1195.8	67.4	5285	8	AAH74866	Aah74866 Nucleotid
c 16	1195.8	67.4	5650	4	ABX94356	Abx94356 Nucleotid
c 17	1195.8	67.4	5650	8	AAF75839	Aaf75839 DNA fragm
c 18	1059.8	59.8	1759	4	AAL57176	Aal57176 Rolling c
c 19	1058.4	59.7	1768	9		Aal57176 Porcine c

c 20	1055.6	59.5	1759	2	AAX35013	Aax35013 Nucvleoti
c 21	1053.2	59.4	3609	4	AAF28320	Aaf28320 pJP107 do
c 22	981.2	55.3	1768	2	AAX35380	Aax35380 Nucleotid
c 23	981.2	55.3	1768	2	AAX35212	Aax35212 Nucleotid
c 24	981.2	55.3	1768	3	AAZ56871	Aaz56871 DNA seque
c 25	981.2	55.3	1768	4	AAF75837	Aaf75837 PCV DNA f
c 26	976.4	55.1	1768	2	AAX35381	Aax35381 Nucleotid
c 27	976.4	55.1	1768	2	AAX35213	Aax35213 Nucleotid
c 28	976.4	55.1	1768	3	AAZ56872	Aaz56872 DNA seque
c 29	976.4	55.1	1768	4	AAF75838	Aaf75838 PCV DNA f
c 30	967.2	54.6	1768	2	AAX35382	Aax35382 Nucleotid
c 31	967.2	54.6	1768	2	AAX35012	Aax35012 Genomic D
c 32	967.2	54.6	1768	2	AAX35214	Aax35214 Nucleotid
c 33	954	53.8	1767	2	AAX35378	Aax35378 Nucleotid
c 34	954	53.8	1767	2	AAX35210	Aax35210 Nucleotid
c 35	954	53.8	1767	3	AAZ56869	Aaz56869 DNA seque
c 36	954	53.8	1767	4	AAF75835	Aaf75835 PCV DNA f
c 37	952.4	53.7	1767	2	AAX35379	Aax35379 Nucleotid
c 38	952.4	53.7	1767	2	AAX35211	Aax35211 Nucleotid
c 39	952.4	53.7	1767	3	AAZ56870	Aaz56870 DNA seque
c 40	952.4	53.7	1767	4	AAF75836	Aaf75836 PCV DNA f
c 41	921	51.9	1759	2	AAX87992	Aax87992 Porcine c
c 42	916.2	51.7	1759	2	AAX83757	Aax83757 Porcine c
c 43	742.2	41.9	1361	2	AAX83755	Aax83755 Nucleotid
c 44	740.6	41.8	1786	2	ABV72527	Abv72527 Nucleotid
c 45	738.4	41.6	1768	8		
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### ALIGNMENTS

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RESULT 1
AAL57177
ID   AAL57177 standard; DNA; 1773 BP.
XX
AC   AAL57177;
XX
DT   27-OCT-2003   (revised)
DT   09-OCT-2003   (first entry)
XX
DE   Porcine circovirus type 1-2 chimeric DNA.
XX
KW   Porcine circovirus type 2; PCV1-2; PCV1; PMWS; weaning piglet; dyspnoea;
KW   progressive weight loss; postweaning multisystemic wasting syndrome; ds;
KW   tachypnea; anaemia; diarrhoea; jaundice; virucide; vaccine; PCV2; gene;
KW   viral infection; chimeric.
XX
OS   Porcine circovirus type 1.
OS   Porcine circovirus type 2.
OS   Chimeric.
XX
FH   Key              Location/Qualifiers
FT   CDS              958..1659"
FT                    /*tag= a
FT                    /product= "Porcine circovirus type 2 ORF2 capsid protein"
XX
PN   WO2003049703-A2.
XX
PD   19-JUN-2003.
XX
PF   11-DEC-2002; 2002WO-US039646.
XX
PR   12-DEC-2001; 2001US-0340775P.
PR   08-NOV-2002; 2002US-0424840P.
PR   09-DEC-2002; 2002US-0314512.
XX
PA   (VIRG ) VIRGINIA TECH INTELLECTUAL PROPERTIES.
PA   (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX
PI   Meng X, Fenaux M, Halbur PG;
XX
DR   WPI; 2003-513959/48.
DR   P-PSDB; AAO23063.
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:     January 24, 2006, 04:27:51 ; Search time 9027 Seconds
                                 (without alignments)
                               11164.666 Million cell updates/sec

Title:        US-10-808-964A-2
Perfect score: 1773
Sequence:     1 ggtaccccgcgtggatggtc.........caaatcggccttcgggtacc 1773

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:        11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     GenEmbl:*
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              10:  gb_sts:*
              11:  gb_sy:*
              12:  gb_un:*
              13:  gb_vi:*
              14:  gb_htg:*
              15:  gb_pl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	
c 1	1386.4	78.2	1768	13	AF264042	AF264042 Porcine c
c 2	1378.4	77.7	1768	13	AF264040	AF264040 Porcine c
c 3	1370.4	77.3	1768	13	AF264039	AF264039 Porcine c
c 4	1370.4	77.3	1768	13	AF520783	AF520783 Porcine c
c 5	1370.4	77.3	1768	13	AF544024	AF544024 Porcine c
c 6	1368.8	77.2	1768	13	AF264041	AF264041 Porcine c
c 7	1367.2	77.1	1768	13	AF264038	AF264038 Porcine c
c 8	1364	76.9	1768	13	AF264043	AF264043 Porcine c
c 9	1364	76.9	1768	13	AF454546	AF454546 Porcine c
c 10	1357.6	76.6	1768	13	AF201309	AF201309 Porcine c
c 11	1346.4	75.9	1768	13	AF201305	AF201305 Porcine c
c 12	1346.4	75.9	1768	13	AF201308	AF201308 Porcine c
c 13	1343.2	75.8	1768	13	AF201306	AF201306 Porcine c
c 14	1341.6	75.7	1768	13	AF201310	AF201310 Porcine c
c 15	1340	75.6	1768	13	AF201307	AF201307 Porcine c
c 16	1306	73.7	1767	11	AJ623306	AJ623306 Synthetic
c 17	1304.4	73.6	1767	13	AF201311	AF201311 Porcine c
c 18	1303.4	73.5	1767	13	AY122275	AY122275 Porcine c

c 19	1301.2	73.4	1767	13	AY288134	AY288134 Porcine c
c 20	1296.4	73.1	1767	13	AY294310	AY294310 Porcine c
c 21	1288.4	72.7	1767	13	AY288133	AY288133 Porcine c
c 22	1285.2	72.5	1768	6	AX379562	AX379562 Sequence
c 23	1285.2	72.5	1768	13	AY099498	AY099498 Porcine c
c 24	1278.8	72.1	1768	6	AX379560	AX379560 Sequence
c 25	1278.8	72.1	1768	13	AY099496	AY099496 Porcine c
c 26	1277.2	72.0	1768	6	AX379564	AX379564 Sequence
c 27	1277.2	72.0	1768	13	AY099500	AY099500 Porcine c
c 28	1274	71.9	1768	6	AX379561	AX379561 Sequence
c 29	1274	71.9	1768	6	AX379563	AX379563 Sequence
c 30	1274	71.9	1768	13	AY099495	AY099495 Porcine c
c 31	1274	71.9	1768	13	AY099499	AY099499 Porcine c
c 32	1262.6	71.2	1759	13	PCCOMGEN	Y09921 Porcine cir
c 33	1261.4	71.1	1768	13	AF305532	AF305532 Porcine c
c 34	1261.4	71.1	1768	13	AF305533	AF305533 Porcine c
c 35	1252	70.6	1762	13	AX379559	AX379559 Sequence
c 36	1252	70.6	1762	13	AY099497	AY099497 Porcine c
c 37	1218.2	68.7	1759	6	AX379565	AX379565 Sequence
c 38	1218.2	68.7	1759	13	AY099501	AY099501 Porcine c
c 39	1196.8	67.5	7400	6	AX226286	AX226286 Sequence
c 40	1195.8	67.4	5225	6	AX226280	AX226280 Sequence
c 41	1195.8	67.4	5650	6	AX226281	AX226281 Sequence
c 42	1059.8	59.8	1759	6	A97282	A97282 Sequence 5
c 43	1059.8	59.8	1759	6	AR145612	AR145612 Sequence
c 44	1059.8	59.8	1759	6	BD081867	BD081867 Porcine c
c 45	1059.8	59.8	1759	6	CQ768117	CQ768117 Sequence

ALIGNMENTS

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RESULT 1
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LOCUS       AF264042    Porcine circovirus type 2 isolate 40895 complete genome.
DEFINITION  Porcine circovirus type 2 isolate 40895 complete genome.
ACCESSION   AF264042
VERSION     AF264042.1  GI:9392644
KEYWORDS    .
SOURCE      Porcine circovirus 2
  ORGANISM  Porcine circovirus 2
            Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE   1  (bases 1 to 1768)
  AUTHORS   Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
  TITLE     Genetic characterization of type 2 porcine circovirus (PCV-2) from
            pigs with postweaning multisystemic wasting syndrome in different
            geographic regions of North America and development of a
            differential PCR-restriction fragment length polymorphism assay to
            detect and differentiate between infections with PCV-1 and PCV-2
  JOURNAL   J. Clin. Microbiol. 38 (7), 2494-2503 (2000)
  PUBMED    10878032
REFERENCE   2  (bases 1 to 1768)
  AUTHORS   Fenaux,M., Halbur,P.G., Gill,M., Toth,T.E. and Meng,X.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-MAY-2000) VMRCVM, Virginia Tech, 1410 Prices Fork
            Road, Blacksburg, VA 24061, USA
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                     /note="Cap"
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